NUTRIPATH · PATIENT REPORT
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NATA Accreditation: #20770

25283-0006

Dr Test Doctor Test Clinic. 123 Test Street, Test Suburb Victoria 3125

Lab ID
Patient ID PAT-100009
Ext ID 25283-0006

Test Patient

Sex: Female • 45yrs • 01-Jan-80
123 Home Street, Test Suburb Vic 3125

RECEIVED
10-Oct-25

COMPREHENSIVE DIGESTIVE STOOL ANALYSIS (CDSA) Level 1

Specimen type - Stool

Collected
05-Oct-25

MACROSCOPIC EXAMINATION

TEST	RESULT
Stool Colour	Green
Stool Form	Semiformed
Mucous	PRESENT

OCCULT BLOOD

TEST	INTERPRETATION
Occult Blood	Negative

TEST	RESULT	H/L	REFERENCE	UNITS
Steatocrit	16.0	H	(0.0-10.0)	%
pH	6.5		(6.3-7.7)	

PATHOGENIC BACTERIA (PCR)

TEST	RESULT
Aeromonas species	DETECTED
Campylobacter species	Not Detected
Salmonella species	Not Detected
Shigella species	Not Detected
Yersinia species	Not Detected

PARASITES (PCR)

TEST	RESULT
Blastocystis hominis	Not Detected
Cryptosporidium species	Not Detected
Dientamoeba fragilis	DETECTED
Entamoeba histolytica	Not Detected
Giardia intestinalis	Not Detected

BACTERIAL CULTURE

Organism	Growth	H/L	Ref Range	Classification
Aeromonas hydrophila	1+	H	(<1+)	PATHOGEN
Citrobacter freundii complex	4+	H	(<4+)	Possible Pathogen
Enterococcus faecium	1+		(<4+)	Non-Pathogen
Klebsiella pneumoniae complex	3+		(<4+)	Non-Pathogen
Pseudomonas aeruginosa	2+		(<4+)	Non-Pathogen
Streptococcus agalactiae	1+		(<4+)	Non-Pathogen

Actinobacteria Phylum Bacteroidetes Phylum Euryarchaeota Phylum Firmicutes Phylum Proteobacteria Phylum Verrucomicrobia Phylum

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BENEFICIAL BACTERIA

TEST	RESULT	H/L	REFERENCE	UNITS
Bifidobacterium animalis	1+		(<4+)	
Bifidobacterium bifidum	2+		(<4+)	
Bifidobacterium breve	NEG		(<4+)	
Bifidobacterium longum	NEG		(<4+)	
Bifid. pseudocatenulatum	NEG		(<4+)	
Enterococcus species	NEG		(<4+)	
Escherichia coli	3+		(<4+)	
Lactobacillus acidophilus	2+		(<4+)	
Lactobacillus casei	2+		(<4+)	
Lactobacillus paracasei	NEG		(<4+)	
Lactobacillus plantarum	NEG		(<4+)	
Lactobacillus rhamnosus	2+		(<4+)	

Actinobacteria Phylum Bacteroidetes Phylum Euryarchaeota Phylum Firmicutes Phylum Proteobacteria Phylum Verrucomicrobia Phylum

Disclaimer: The results presented for culture-based microbiome analyses are intended for clinical interpretation and research purposes. Culture methods are limited in detecting the full microbial diversity present in a specimen; some organisms may be unculturable under standard laboratory conditions.

Only tests and analytes explicitly listed in the laboratory's accredited scope are covered under accreditation. Clinicians are encouraged to consult the governing accrediting body's publicly available scope for confirmation of accredited analytes and methods.

Results should be interpreted in the context of clinical findings, patient history, and complementary diagnostic information. The laboratory does not guarantee detection of all organisms in a specimen, and negative results do not rule out the presence of unculturable or fastidious species.

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SUSCEPTIBILITY - BACTERIA

Antimicrobials	Aeromonas hydrophila Susceptible	Citrobacter freundii complex Susceptible	Klebsiella pneumoniae complex Susceptible	Pseudomonas aeruginosa Susceptible
Ampicillin	R	S	R	NT
Augmentin	S	R	S	NT
Ciprofloxacin	S	S	S	R
Gentamicin	S	S	S	NT
Meropenem	S	S	S	S
Norfloxacin	S	S	S	NT
Trimethoprim/Sulpha	S	S	S	NT

R Resistant S Susceptible I Intermediate NT Not Tested

Disclaimer: The antibiotics listed have been reported as requested by the treating healthcare practitioner. Clinical necessity for antibiotic use may vary, and prescription should be based on the professional judgment of the healthcare practitioner and patient case. Information regarding natural inhibitors is provided for reference purposes only and is not intended to replace medical advice or treatment.

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NATURAL INHIBITORS - BACTERIA

Citrobacter freundii complex	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed		
Coptis		
Garlic		
Golden Seal		
Oregano		

Klebsiella pneumoniae complex	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed		
Coptis		
Garlic		
Golden Seal		
Oregano		

Streptococcus agalactiae	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed		
Coptis		
Garlic		
Golden Seal		
Oregano		

NATURAL INHIBITORS - BACTERIA

Pseudomonas aeruginosa	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed		
Coptis		
Garlic		
Golden Seal		
Oregano		

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MYCOLOGY CULTURE

Organism	Growth	H/L	Ref Range	Classification
Candida albicans	2+	H	(<2+)	Possible Pathogen
Candida parapsilosis	1+		(<2+)	Non-Pathogen

SUSCEPTIBILITY - MYCOLOGY

Antimicrobials	Candida albicans Susceptible
Fluconazole	R
Voriconazole	S

R Resistant S Susceptible I Intermediate NT Not Tested

NATURAL INHIBITORS - MYCOLOGY

Candida albicans	Low Inhibition	High Inhibition
Nystatin		
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed		
Coptis		
Garlic		
Golden Seal		
Oregano		

NATURAL INHIBITORS - MYCOLOGY

Candida parapsilosis	Low Inhibition	High Inhibition
Nystatin		
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed		
Coptis		
Garlic		
Golden Seal		
Oregano		

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The Four "R" Treatment Protocol

REMOVE	Using a course of antimicrobial, antibacterial, antiviral or anti parasitic therapies in cases where organisms are present. It may also be necessary to remove offending foods, gluten, or medication that may be acting as antagonists. Consider testing IgG96 foods as a tool for removing offending foods.	ANTIMICROBIAL	Oil of oregano, berberine, caprylic acid
		ANTIBACTERIAL	Liquorice, zinc carnosine, mastic gum, tribulus, berberine, black walnut, caprylic acid, oil of oregano
		ANTIFUNGAL	Oil of oregano, caprylic acid, berberine, black walnut
		ANTIPARASITIC	Artemesia, black walnut, berberine, oil of oregano
		ANTIVIRAL	Cat's claw, berberine, echinacea, vitamin C, vitamin D3, zinc, reishi mushrooms
		BIOFILM	Oil of oregano, protease
REPLACE	In cases of maldigestion or malabsorption, it may be necessary to restore proper digestion by supplementing with digestive enzymes.	DIGESTIVE SUPPORT	Betaine hydrochloride, tilactase, amylase, lipase, protease, apple cider vinegar, herbal bitters
REINOCULATE	Recolonisation with healthy, beneficial bacteria. Supplementation with probiotics, along with the use of prebiotics helps re-establish the proper microbial balance.	PREBIOTICS	Slippery elm, pectin, larch arabinogalactans
		PROBIOTICS	Bifidobacterium animalis sup lactose, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius sup salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccaromyces boulardii
REPAIR & REBALANCE	Restore the integrity of the gut mucosa by giving support to healthy mucosal cells, as well as immune support. Address whole body health and lifestyle factors so as to prevent future GI dysfunction.	INTESTINAL MUCOSA IMMUNE SUPPORT	Saccaromyces boulardii, lauric acid
		INTESTINAL BARRIER REPAIR	L-Glutamine, aloe vera, liquorice, marshmallow root, okra, quercetin, slippery elm, zinc carnosine, Saccaromyces boulardii, omega 3 essential fatty acids, B vitamins
		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management

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Macroscopy/Microscopy Comment

SEMI-FORMED STOOL:

A SEMI-FORMED stool specimen classified as Type 4 on the Bristol Stool Chart is generally considered optimal, indicating balanced gut motility, adequate hydration, and sufficient dietary fibre intake. This stool consistency is often associated with efficient digestion, proper colonic function, and microbial stability. However, while Type 4 stools typically suggest gastrointestinal homeostasis, they do not always correlate with a healthy gut microbiome. Pathogenic bacteria, viral infections, parasitic infestations, or gut dysbiosis may still be present, even in well-formed stools. Clinical recommendations include maintaining a fiber-rich diet with prebiotic and probiotic sources, ensuring consistent hydration, and promoting gut microbial diversity through fermented foods or supplementation.

MUCOUS HAS BEEN DETECTED IN THIS SPECIMEN:

The presence of mucous in the stool may be due to prolonged irritation of the intestinal mucosa. An increase of visible mucous may also be reflective of an inflammatory gastrointestinal condition such as: Crohns, Ulcerative colitis, irritable bowel syndrome (IBS) and infection.
Treatment:

- Investigate and treat possible underlying cause.
- Assess other Gut markers (e.g. calprotectin, M2PK, etc).

FAECAL OCCULT BLOOD NEGATIVE:

Faecal occult blood has not been detected in this specimen. If the test result is negative and clinical symptoms persist, additional follow-up testing using other clinical methods is recommended.

GIT Markers Comment

ELEVATED STEATOCRIT:

The presence of steatorrhea is an indirect indicator of incomplete fat digestion. Consider high dietary fat intake, cholestasis, malabsorption and digestion (diarrhoea, pancreatic or bile salt insufficiency), intestinal dysbiosis, parasites, NSAIDs use, short bowel syndrome, whipple disease, crohn's disease, food allergies & sensitivities.

Treatment:

o Prebiotic and probiotic supplementation

o Supplement hydrochloride, digestive enzymes or other digestive aids

o Investigate underlying causes

o Investigate food sensitivities and allergies

o Remove potential irritants

o Review markers such as pancreatic elastase 1 and calprotectin

Microorganism Summary

AEROMONAS SPECIES DETECTED by PCR

DNA consistent with the presence of Aeromonas species has been detected using PCR techniques.

Aeromonas have been implicated as a cause of both acute and persistent diarrhoeal illness (usually watery) and may be accompanied by fever and/or abdominal pain. Aeromonas is widely distributed in the freshwater, esturaine and marine environments and infection usually occurs in the summer months.

TREATMENT SUGGESTIONS:

Most cases of Aeromonas-associated diarrhoea are self-limited and can be managed with supportive therapy. If treatment is considered necessary, Aeromonas spp. are usually sensitive to Trimethoprim-Sulphamethoxazole and Fluoroquinolones. Sensitivity to tetracycline is variable.

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Rule out allergy to above medication before prescribing/taking. Consult ID specialist if patient is showing severe symptoms or immunocompromised.

DIENTAMOEBA FRAGILIS DETECTED by PCR.

DNA consistent with the presence of Dientamoeba fragilis has been detected using PCR techniques.

Dientamoeba fragilis appears to be extremely common and may have a cosmopolitan distribution, although there are large variations in prevalence. Dientamoeba fragilis has been linked to intestinal symptoms, especially in children. The most common symptoms associated with this organism are abdominal pain, intermittent diarrhoea, bloating and anorexia.

TREATMENT SUGGESTIONS:

Mild symptoms are self-limiting.

If treatment is warranted, metronidazole for 10 days or a single 2g dose of Tinidazole may be used. Tetracycline has also proven effective in adults.

Rule out allergy to above medication before prescribing/taking. Consult ID specialist if patient is showing severe symptoms or immunocompromised.

AEROMONAS SPECIES: PHYLUM: Proteobacteria

Aeromonas species are Gram-negative bacteria belonging to the phylum Proteobacteria. While primarily found in aquatic environments, some Aeromonas species are transient or opportunistic members of the human gut microbiome. In healthy individuals, their presence is generally low, but in immunocompromised hosts or those with gut dysbiosis, species such as A. hydrophila and A. caviae can cause gastrointestinal infections, leading to symptoms like diarrhea and abdominal pain (Janda and Abbott, 2010). Aeromonas species are also notable for their ability to acquire and disseminate antimicrobial resistance genes, posing a risk in environments with frequent antibiotic use (Pablos et al., 2010). Although their exact role in the gut microbiome is not fully understood, monitoring these bacteria is crucial in assessing their impact on microbial diversity and potential for opportunistic infections.

CITROBACTER FREUNDII COMPLEX: PHYLUM: Proteobacteria

Citrobacter freundii complex consists of several species including C. freundii, C. braakii, C. gillenii, C. murliniae, C. sedlakii, C. werkmanii and C. youngae and are Gram-negative bacteria from the phylum Proteobacteria and is a common resident of the human gut microbiome. Typically found as a commensal organism, C. freundii plays a minor role in maintaining microbial diversity within the gut. However, it is also an opportunistic pathogen, particularly in immunocompromised individuals, and has been linked to infections such as urinary tract infections, pneumonia, and bacteremia (Whalen et al., 2007). In the context of gut health, C. freundii generally poses little risk, but during episodes of dysbiosis or antibiotic treatment, its population can increase, leading to potential infections. Its ability to acquire antibiotic resistance, especially through horizontal gene transfer, makes it a clinical concern when overgrowth occurs. Monitoring C. freundii in gut microbiome studies is essential for understanding its role in both health and disease.

ENTEROCOCCUS FAECIUM: PHYLUM: Firmicutes

Enterococcus faecium is a Gram-positive bacterium from the phylum Firmicutes and is commonly found in the human gut microbiome. While it generally functions as a commensal organism, contributing to microbial diversity and gut homeostasis, E. faecium is also a significant opportunistic pathogen. It is known for causing infections such as bacteremia, endocarditis, and urinary tract infections, particularly in immunocompromised individuals or during gut dysbiosis (Arias and Murray, 2012). A major concern with E. faecium is its high level of antibiotic resistance, especially to vancomycin, which has made it a major healthcare-associated pathogen. Its ability to acquire and transfer resistance genes elevates its clinical importance. While it plays a normal role in the gut microbiome, monitoring its levels is critical for preventing healthcare-related infections.

KLEBSIELLA PNEUMONIAE COMPLEX: PHYLUM: Proteobacteria

Klebsiella pneumoniae complex consists of seven closely related species including the most frequently isolated K. pneumoniae, K. variicola and K. quasipneumoniae and are Gram-negative bacteria from the phylum Proteobacteria and is a common member of the human gut microbiome. While it generally exists as a commensal organism, it can become an opportunistic pathogen, particularly in

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immunocompromised individuals or during gut dysbiosis. K. pneumoniae is a significant cause of healthcare-associated infections, including pneumonia, urinary tract infections, septicemia, and liver abscesses (Podschun and Ullmann, 1998). In the gut, K. pneumoniae contributes to microbial diversity, but its overgrowth or translocation can lead to severe infections. It is particularly concerning due to its ability to develop antibiotic resistance, including carbapenem-resistant strains, making it a major clinical threat (Pitout et al., 2015). Monitoring K. pneumoniae in the gut microbiome is crucial for understanding its role in both health and infection risk.

PSEUDOMONAS AERUGINOSA: PHYLUM: Proteobacteria

Pseudomonas aeruginosa is a Gram-negative bacterium commonly known for its opportunistic pathogenicity. While it is primarily associated with infections in immunocompromised patients and chronic infections such as cystic fibrosis, its presence in the gut microbiome is less well-characterized. In the gut, P. aeruginosa can be part of the microbial community, often as a transient or minor member. Its potential impact on gut health includes interactions with other gut microbiota, which could influence inflammation and microbial balance (Pang et al., 2019). Despite its role as a pathogen, understanding its dynamics within the gut microbiome could offer insights into its broader ecological roles and impact on gastrointestinal health (Kresse et al., 2018).

STREPTOCOCCUS AGALACTIAE: Phylum: Firmicutes

Streptococcus agalactiae is a Gram-positive bacterium commonly found in the human gut microbiome. It is part of the group known as beta-hemolytic streptococci. While S. agalactiae is predominantly recognized for its role as a pathogen causing infections in neonates, pregnant women, and immunocompromised individuals, it is also a normal component of the gut microbiota. Within the gut, S. agalactiae may influence microbial diversity and contribute to the overall balance of the gut flora. Its presence in the gut microbiome is linked to potential impacts on gut health and immune responses, though its pathogenic potential under certain conditions is well-documented (Schrag et al., 2002; Kline et al., 2011).

CANDIDA PARAPSILOSIS: PHYLUM: Ascomycota

Candida parapsilosis is a yeast from the phylum Ascomycota and is a part of the human gut microbiome. Typically found in low abundance, it can act as a commensal organism but has the potential to become opportunistic, particularly in immunocompromised individuals or those undergoing gut dysbiosis (Tavanti et al., 2005). C. parapsilosis is often associated with invasive infections, such as fungemia, especially in hospital settings, where it can cause catheter-related bloodstream infections. In the gut microbiome, its role is generally minor, but its ability to form biofilms and resist certain antifungal agents makes it a concern when overgrowth occurs. Monitoring C. parapsilosis levels in the gut is important for understanding its potential contribution to infection, particularly in vulnerable populations.

BIFIDOBACTERIUM ANIMALIS LOW:

Bifidobacterium animalis is a Gram-positive bacterium from the phylum Actinobacteria and is a prominent member of the human gut microbiome, particularly known for its probiotic properties. It is commonly used in commercial probiotic products, especially the subspecies B. animalis subsp. lactis, due to its ability to survive the acidic environment of the stomach and colonize the intestines (Turroni et al., 2011). In the gut, B. animalis plays a critical role in breaking down complex carbohydrates and producing short-chain fatty acids, which promote gut health by supporting the intestinal barrier and modulating inflammation (Rivière et al., 2014). Its presence has been linked to improved digestive health, enhanced immune function, and potential benefits in reducing symptoms of gastrointestinal disorders. Monitoring B. animalis in the gut microbiome is essential for understanding its role in maintaining gut homeostasis and overall health.

BIFIDOBACTERIUM BREVE:

Bifidobacterium breve is a Gram-positive bacterium within the phylum Actinobacteria, commonly found in the gut microbiome of infants and adults. It is a key player in early gut colonization, particularly in breastfed infants, where it helps digest human milk oligosaccharides and supports the development of the immune system (Turroni et al., 2012). In the adult gut, B. breve contributes to the fermentation of complex carbohydrates, producing short-chain fatty acids such as butyrate, which promote gut health by enhancing the intestinal barrier and reducing inflammation (Rivière et al., 2014). Its probiotic properties have been associated with various health benefits, including improved digestion, protection against pathogens, and potential roles in managing conditions such as irritable bowel syndrome (IBS). Monitoring B. breve levels can provide insights into its role in maintaining a healthy gut microbiome.

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BIFIDOBACTERIUM LONGUM LOW:

Bifidobacterium longum is a Gram-positive bacterium from the phylum Actinobacteria and is a prominent member of the human gut microbiome. Found in both infants and adults, B. longum plays a crucial role in fermenting complex carbohydrates, including dietary fibers and human milk oligosaccharides, to produce short-chain fatty acids, such as acetate and lactate, that promote gut health (O'Callaghan and van Sinderen, 2016). This species is associated with several health benefits, including enhancing gut barrier function, modulating the immune system, and protecting against gastrointestinal pathogens. Its probiotic properties make it a key component in many probiotic supplements aimed at improving digestion and alleviating symptoms of disorders like irritable bowel syndrome (Rivière et al., 2014). Monitoring B. longum in gut microbiome studies helps assess its contribution to microbial balance and overall health.

BIFIDOBACTERIUM PSEUDOCATENULATUM LOW:

Bifidobacterium pseudocatenulatum is a Gram-positive bacterium belonging to the phylum Actinobacteria and is a common member of the human gut microbiome. It is particularly abundant in infants but persists into adulthood, contributing to gut health by fermenting dietary fibers and producing short-chain fatty acids such as acetate, which support intestinal barrier function and reduce inflammation (Rivière et al., 2014). Recent studies have shown that B. pseudocatenulatum has potential probiotic properties, including modulating immune responses and inhibiting the growth of harmful pathogens in the gut (O'Callaghan and van Sinderen, 2016). Its role in gut microbiota is associated with maintaining microbial diversity and promoting a balanced gut environment, making it a promising candidate for therapeutic interventions aimed at improving gut health and managing gastrointestinal disorders.

ESCHERICHIA COLI:

Escherichia coli (E. coli) is a Gram-negative bacterium belonging to the phylum Proteobacteria and is a key component of the human gut microbiome. Most strains of E. coli are commensal, contributing to normal gut functions such as vitamin K production and preventing colonization by pathogenic bacteria. It plays a crucial role in maintaining gut homeostasis and microbial diversity (Tenaillon et al., 2010). However, certain strains of E. coli can become pathogenic, leading to gastrointestinal diseases such as diarrhea, urinary tract infections, and more severe conditions like hemolytic uremic syndrome. Pathogenic strains, such as enterohemorrhagic E. coli (EHEC), can produce toxins like Shiga toxin, which can cause serious infections (Kaper et al., 2004). While most E. coli strains are beneficial, monitoring its pathogenic variants is important for maintaining gut health.

LACTOBACILLUS PLANTARUM LOW:

Lactobacillus plantarum is a Gram-positive bacterium from the phylum Firmicutes, prominently present in the human gut microbiome. Known for its probiotic properties, L. plantarum contributes to gut health by fermenting dietary fibers into lactic acid, which lowers intestinal pH and inhibits the growth of harmful microorganisms (Hammes & Hertel, 2009). This species is also involved in maintaining the integrity of the gut barrier and modulating immune responses, which can help prevent or alleviate gastrointestinal disorders such as irritable bowel syndrome (IBS) and inflammatory bowel disease (IBD) (O'Callaghan & van Sinderen, 2016). Its ability to adhere to the gut lining and produce antimicrobial peptides makes L. plantarum a valuable component of a healthy gut microbiota.

Methodology

Automated Chemistry/Immunochemistry, Microscopy, pH Electrode, MALDI-TOF (Matrix-Assisted Laser Desorption/Ionization Time of Flight), Polymerase Chain Reaction (PCR), Quantitative PCR (qPCR)

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